

SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY CORPORATION

<120> High-Affinity Choline Transporter

<130> A011-05PCT

<140>

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<150> JP 11/240642

<151> 1999-08-27

<150> JP 11/368991

<151> 1999-12-27

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 1731

<212> DNA

<213> Caenorhabditis elegans

<220>

<221> CDS

<222> (1)..(1731)

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gag ctt gaa tca gaa gcc ggc gcg gcg acg gaa gag gtg atg ita gct 144
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ggg aga aac atc gga act ctt gtc gga att ttc aca atg act gcc acg 192
 Gly Arg Asn Ile Gly Thr Leu Val Gly Ile Phe Thr Met Thr Ala Thr
 50 55 60

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 Val Met Gly Gly Leu Leu Phe Ala Lys Lys Met Arg Glu Glu Gly Tyr
 100 105 110

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 Ile Thr Met Leu Asp Pro Phe Gln His Lys Tyr Gly Gln Arg Ile Gly
 115 120 125

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 Gly Leu Met Tyr Val Pro Ala Leu Leu Gly Glu Thr Phe Trp Thr Ala
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 195 200 205

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 210 215 220

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 225 230 235 240

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 Val Leu Ser Ser Lys Thr Ala His Gly Ala Gln Thr Leu Ser Phe Val
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Val Val Pro Leu Val Phe Gln Tyr Leu Thr Pro Arg Trp Val Ala Phe			
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Ile Gly Leu Gly Ala Val Ser Ala Ala Val Met Ser Ser Ala Asp Ser			
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Ile Ala Ile Ile Cys Val Gly Ile Met Ala Thr Ile Met Ala Leu Thr			
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Ile Gln Ser Ile Tyr Gly Leu Trp Tyr Leu Cys Ala Asp Leu Val Tyr			
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Val Ile Leu Phe Pro Gln Leu Leu Cys Val Val Tyr Met Pro Arg Ser			
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Asn Thr Tyr Gly Ser Leu Ala Gly Tyr Ala Val Gly Leu Val Leu Arg
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 Pro Met Tyr Thr Asp Gly Val Gln Tyr Phe Pro Phe Arg Thr Thr Ala
 465 470 475 480

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 485 490 495

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 Cys Val Val Asn Ile Pro Ile Asp His Val Pro Leu Pro Ser Asp Val
 515 520 525

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 Ser Phe Ala Val Ser Ser Glu Thr Leu Asn Met Lys Ala Pro Asn Gly
 530 535 540

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 545 550 555 560

tta tta cat cca tat tgc gac caa agt tat tat tcc aca aat agc aat 1728
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1731

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<211> 576

<212> PRT

<213> Caenorhabditis elegans

<400> 2

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 35 40 45
 Gly Arg Asn Ile Gly Thr Leu Val Gly Ile Phe Thr Met Thr Ala Thr
 50 55 60
 Trp Val Gly Gly Ala Tyr Ile Asn Gly Thr Ala Glu Ala Leu Tyr Asn
 65 70 75 80
 Gly Gly Leu Leu Gly Cys Gln Ala Pro Val Gly Tyr Ala Ile Ser Leu
 85 90 95
 Val Met Gly Gly Leu Leu Phe Ala Lys Lys Met Arg Glu Glu Gly Tyr
 100 105 110
 Ile Thr Met Leu Asp Pro Phe Gln His Lys Tyr Gly Gln Arg Ile Gly
 115 120 125
 Gly Leu Met Tyr Val Pro Ala Leu Leu Gly Glu Thr Phe Trp Thr Ala
 130 135 140
 Ala Ile Leu Ser Ala Leu Gly Ala Thr Leu Ser Val Ile Leu Gly Ile
 145 150 155 160
 Asp Met Asn Ala Ser Val Thr Leu Ser Ala Cys Ile Ala Val Phe Tyr
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 Thr Phe Thr Gly Gly Tyr Tyr Ala Val Ala Tyr Thr Asp Val Val Gln
 180 185 190
 Leu Phe Cys Ile Phe Val Gly Leu Trp Val Cys Val Pro Ala Ala Met

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Ala Ile Ala Arg Asn Thr Asp Trp Arg Met Thr Asp Tyr Ser Pro Trp		
290	295	300
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Thr Ile Arg Pro His Ala Ser Glu Lys Glu Val Ile Ile Val Met Arg		
370	375	380
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385	390	395
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Leu Ile Gly Gly Glu Pro Leu Val Ser Leu Pro Ala Phe Phe His Tyr		
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8 / 29

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Gly Leu Ala Trp Ala Gln Ala Pro Ile Gly Tyr Ser Leu Ser Leu Ile			
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Leu Gly Gly Leu Phe Phe Ala Lys Pro Met Arg Ser Lys Gly Tyr Val			
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Thr Met Leu Asp Pro Phe Gln Gln Ile Tyr Gly Lys Arg Met Gly Gly			
115	120	125	
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Val Asn Ile Ser Val Ile Val Ser Ala Leu Ile Ala Ile Leu Tyr Thr			
165	170	175	
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 195 200 205

cat cct gca gtc acc gac att gga ttc act gct gig cat gct aaa tac 672
 His Pro Ala Val Thr Asp Ile Gly Phe Thr Ala Val His Ala Lys Tyr
 210 215 220

cag agt ccc tgg ctg gga acc att gaa tca gtt gaa gtc tac acc tgg 720
 Gln Ser Pro Trp Leu Gly Thr Ile Glu Ser Val Glu Val Tyr Thr Trp
 225 230 235 240

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 260 265 270

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 Tyr Gly Phe Pro Asp Pro Lys Thr Lys Glu Glu Ala Asp Met Ile Leu
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ccg att gtt cta cag tac ctc tgc cct gtg tac att tcc ttc ttt ggg 1008
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 355 360 365

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 Tyr Gly Ala Val Ala Gly Tyr Ile Phe Gly Leu Phe Leu Arg Ile Thr
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 450 455 460

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 515 520 525

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 545 550 555 560

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<211> 580

<212> PRT

<213> Rattus norvegicus

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 65 70 75 80
 Gly Leu Ala Trp Ala Gln Ala Pro Ile Gly Tyr Ser Leu Ser Leu Ile
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 100 105 110
 Thr Met Leu Asp Pro Phe Gln Gln Ile Tyr Gly Lys Arg Met Gly Gly
 115 120 125
 Leu Leu Phe Ile Pro Ala Leu Met Gly Glu Met Phe Trp Ala Ala Ala
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 Ile Phe Ser Ala Leu Gly Ala Thr Ile Ser Val Ile Ile Asp Val Asp
 145 150 155 160
 Val Asn Ile Ser Val Ile Val Ser Ala Leu Ile Ala Ile Leu Tyr Thr
 165 170 175
 Leu Val Gly Gly Leu Tyr Ser Val Ala Tyr Thr Asp Val Val Gln Leu
 180 185 190
 Phe Cys Ile Phe Ile Gly Leu Trp Ile Ser Val Pro Phe Ala Leu Ser
 195 200 205
 His Pro Ala Val Thr Asp Ile Gly Phe Thr Ala Val His Ala Lys Tyr
 210 215 220
 Gln Ser Pro Trp Leu Gly Thr Ile Glu Ser Val Glu Val Tyr Thr Trp
 225 230 235 240

Leu Asp Asn Phe Leu Leu Leu Met Leu Gly Gly Ile Pro Trp Gln Ala
 245 250 255
 Tyr Phe Gln Arg Val Leu Ser Ser Ser Ser Ala Thr Tyr Ala Gln Val
 260 265 270
 Leu Ser Phe Leu Ala Ala Phe Gly Cys Leu Val Met Ala Leu Pro Ala
 275 280 285
 Ile Cys Ile Gly Ala Ile Gly Ala Ser Thr Asp Trp Asn Gln Thr Ala
 290 295 300
 Tyr Gly Phe Pro Asp Pro Lys Thr Lys Glu Glu Ala Asp Met Ile Leu
 305 310 315 320
 Pro Ile Val Leu Gln Tyr Leu Cys Pro Val Tyr Ile Ser Phe Phe Gly
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 Leu Gly Ala Val Ser Ala Ala Val Met Ser Ser Ala Asp Ser Ser Ile
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 Leu Ser Ala Ser Ser Met Phe Ala Arg Asn Ile Tyr Gln Leu Ser Phe
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 Arg Gln Asn Ala Ser Asp Lys Glu Ile Val Trp Val Met Arg Ile Thr
 370 375 380
 Val Phe Val Phe Gly Ala Ser Ala Thr Ala Met Ala Leu Leu Thr Lys
 385 390 395 400
 Thr Val Tyr Gly Leu Trp Tyr Leu Ser Ser Asp Leu Val Tyr Ile Ile
 405 410 415
 Ile Phe Pro Gln Leu Leu Cys Val Leu Phe Ile Lys Gly Thr Asn Thr
 420 425 430
 Tyr Gly Ala Val Ala Gly Tyr Ile Phe Gly Leu Phe Leu Arg Ile Thr
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 465 470 475 480
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 485 490 495
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 Ile Phe Asp Ala Val Val Ser Arg His Ser Glu Glu Asn Met Asp Lys

515 520 525
 Thr Ile Leu Val Arg Asn Glu Asn Ile Lys Leu Asn Glu Leu Ala Pro
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 Val Lys Pro Arg Gln Ser Leu Thr Leu Ser Ser Thr Phe Thr Asn Lys
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 20 25 30

 ggc agc gca gaa gag cgc agc gaa gcc atc ata gtt ggt ggc cga gat 144
 Gly Ser Ala Glu Glu Arg Ser Glu Ala Ile Ile Val Gly Gly Arg Asp
 35 40 45

 att ggt tta ttg gtt ggt gga ttt acc atg aca gct acc tgg gtc gga 192

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Ile Gly Leu Leu Val Gly Gly Phe Thr Met Thr Ala Thr Trp Val Gly
 50 55 60

gga ggg tat atc aat ggc aca gct gaa gca gtt tat gla cca ggt tat 240
 Gly Gly Tyr Ile Asn Gly Thr Ala Glu Ala Val Tyr Val Pro Gly Tyr
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 Gly Leu Ala Trp Ala Gln Ala Pro Ile Gly Tyr Ser Leu Ser Leu Ile
 85 90 95

tta ggt ggc ctg ttc ttt gca aaa cct atg cgt tca aag ggg tat gtg 336
 Leu Gly Gly Leu Phe Phe Ala Lys Pro Met Arg Ser Lys Gly Tyr Val
 100 105 110

acc atg tta gac ccg ttt cag caa atc tat gga aaa cgc atg ggc gga 384
 Thr Met Leu Asp Pro Phe Gln Gln Ile Tyr Gly Lys Arg Met Gly Gly
 115 120 125

ctc ctg ttt att cct gca ctg atg gga gaa atg ttc tgg gct gca gca 432
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 145 150 155 160

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 Met His Ile Ser Val Ile Ile Ser Ala Leu Ile Ala Thr Leu Tyr Thr
 165 170 175

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 180 185 190

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 210 215 220

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 Gln Lys Pro Trp Leu Gly Thr Val Asp Ser Ser Glu Val Tyr Ser Trp
 225 230 235 240

ctt gat agt ttt ctg ttg ttg atg ctg ggt gga atc cca tgg caa gca 768
 Leu Asp Ser Phe Leu Leu Leu Met Leu Gly Gly Ile Pro Trp Gln Ala
 245 250 255

tac ttt cag agg gtt ctg tct tct tcc tca gcc acc tat gct caa gtg 816
 Tyr Phe Gln Arg Val Leu Ser Ser Ser Ser Ala Thr Tyr Ala Gln Val
 260 265 270

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 275 280 285

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 Ile Leu Ile Gly Ala Ile Gly Ala Ser Thr Asp Trp Asn Gln Thr Ala
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 Tyr Gly Leu Pro Asp Pro Lys Thr Thr Glu Glu Ala Asp Met Ile Leu
 305 310 315 320

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 Pro Ile Val Leu Gln Tyr Leu Cys Pro Val Tyr Ile Ser Phe Phe Gly
 325 330 335

ctt ggt gca gtt tct gct gct gtt atg tca tca gca gat tct tcc atc 1056
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340

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350

tig tca gca agt tcc atg ttt gca cgg aac atc tac cag ctt tcc ttc 1104
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365

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375

380

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390

395

400

act gtg tat ggg ctc tgg tac ctc agt tct gac ctt gtt tac atc gtt 1248
 Thr Val Tyr Gly Leu Trp Tyr Leu Ser Ser Asp Leu Val Tyr Ile Val

405

410

415

atc ttc ccc cag ctg ctt tgt gta ctc ttt gtt aag gga acc aac acc 1296
 Ile Phe Pro Gln Leu Leu Cys Val Leu Phe Val Lys Gly Thr Asn Thr

420

425

430

tat ggg gcc gtg gca ggt tat gtt tct ggc ctc ttc ctg aga ata act 1344
 Tyr Gly Ala Val Ala Gly Tyr Val Ser Gly Leu Phe Leu Arg Ile Thr

435

440

445

gga ggg gag cca tat ctg tat ctt cag ccc ttg atc ttc tac cct ggc 1392
 Gly Gly Glu Pro Tyr Leu Tyr Leu Gln Pro Leu Ile Phe Tyr Pro Gly

450

455

460

tat tac cct gat gat aat ggt ata tat aat cag aaa ttt cca ttt aaa 1440
 Tyr Tyr Pro Asp Asp Asn Gly Ile Tyr Asn Gln Lys Phe Pro Phe Lys

465	470	475	480	
aca ctt gcc atg gtt aca tca ttc tta acc aac att tgc atc tcc tat				1488
Thr Leu Ala Met Val Thr Ser Phe Leu Thr Asn Ile Cys Ile Ser Tyr				
	485	490	495	
cia gcc aag tat cia ttt gaa agt gga acc ttg cca cct aaa tta gat				1536
Leu Ala Lys Tyr Leu Phe Glu Ser Gly Thr Leu Pro Pro Lys Leu Asp				
	500	505	510	
gta ttt gat gct gtt gtt gca aga cac agt gaa gaa aac atg gat aag				1584
Val Phe Asp Ala Val Val Ala Arg His Ser Glu Glu Asn Met Asp Lys				
	515	520	525	
aca att ctt gtc aaa aat gaa aat att aaa tta gat gaa ctt gca ctt				1632
Thr Ile Leu Val Lys Asn Glu Asn Ile Lys Leu Asp Glu Leu Ala Leu				
	530	535	540	
gtg aag cca cga cag agc atg acc ctc agc tca act ttc acc aat aaa				1680
Val Lys Pro Arg Gln Ser Met Thr Leu Ser Ser Thr Phe Thr Asn Lys				
	545	550	555	560
gag gcc ttc ctt gat gtt gat tcc agt cca gaa ggg tct ggg act gaa				1728
Glu Ala Phe Leu Asp Val Asp Ser Ser Pro Glu Gly Ser Gly Thr Glu				
	565	570	575	
gat aat tta cag tga				1743
Asp Asn Leu Gln				
	580			

<210> 6

<211> 580

<212> PRT

<213> Homo sapiens

<400> 6

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 Gly Ser Ala Glu Glu Arg Ser Glu Ala Ile Ile Val Gly Gly Arg Asp
 35 40 45
 Ile Gly Leu Leu Val Gly Gly Phe Thr Met Thr Ala Thr Trp Val Gly
 50 55 60
 Gly Gly Tyr Ile Asn Gly Thr Ala Glu Ala Val Tyr Val Pro Gly Tyr
 65 70 75 80
 Gly Leu Ala Trp Ala Gln Ala Pro Ile Gly Tyr Ser Leu Ser Leu Ile
 85 90 95
 Leu Gly Gly Leu Phe Phe Ala Lys Pro Met Arg Ser Lys Gly Tyr Val
 100 105 110
 Thr Met Leu Asp Pro Phe Gln Gln Ile Tyr Gly Lys Arg Met Gly Gly
 115 120 125
 Leu Leu Phe Ile Pro Ala Leu Met Gly Glu Met Phe Trp Ala Ala Ala
 130 135 140
 Ile Phe Ser Ala Leu Gly Ala Thr Ile Ser Val Ile Ile Asp Val Asp
 145 150 155 160
 Met His Ile Ser Val Ile Ile Ser Ala Leu Ile Ala Thr Leu Tyr Thr
 165 170 175
 Leu Val Gly Gly Leu Tyr Ser Val Ala Tyr Thr Asp Val Val Gln Leu
 180 185 190
 Phe Cys Ile Phe Val Gly Leu Trp Ile Ser Val Pro Phe Ala Leu Ser
 195 200 205
 His Pro Ala Val Ala Asp Ile Gly Phe Thr Ala Val His Ala Lys Tyr
 210 215 220
 Gln Lys Pro Trp Leu Gly Thr Val Asp Ser Ser Glu Val Tyr Ser Trp
 225 230 235 240
 Leu Asp Ser Phe Leu Leu Leu Met Leu Gly Gly Ile Pro Trp Gln Ala
 245 250 255
 Tyr Phe Gln Arg Val Leu Ser Ser Ser Ser Ala Thr Tyr Ala Gln Val

260	265	270
Leu Ser Phe Leu Ala Ala Phe Gly Cys Leu Val Met Ala Ile Pro Ala		
275	280	285
Ile Leu Ile Gly Ala Ile Gly Ala Ser Thr Asp Trp Asn Gln Thr Ala		
290	295	300
Tyr Gly Leu Pro Asp Pro Lys Thr Thr Glu Glu Ala Asp Met Ile Leu		
305	310	315
Pro Ile Val Leu Gln Tyr Leu Cys Pro Val Tyr Ile Ser Phe Phe Gly		
325	330	335
Leu Gly Ala Val Ser Ala Ala Val Met Ser Ser Ala Asp Ser Ser Ile		
340	345	350
Leu Ser Ala Ser Ser Met Phe Ala Arg Asn Ile Tyr Gln Leu Ser Phe		
355	360	365
Arg Gln Asn Ala Ser Asp Lys Glu Ile Val Trp Val Met Arg Ile Thr		
370	375	380
Val Phe Val Phe Gly Ala Ser Ala Thr Ala Met Ala Leu Leu Thr Lys		
385	390	395
Thr Val Tyr Gly Leu Trp Tyr Leu Ser Ser Asp Leu Val Tyr Ile Val		
405	410	415
Ile Phe Pro Gln Leu Leu Cys Val Leu Phe Val Lys Gly Thr Asn Thr		
420	425	430
Tyr Gly Ala Val Ala Gly Tyr Val Ser Gly Leu Phe Leu Arg Ile Thr		
435	440	445
Gly Gly Glu Pro Tyr Leu Tyr Leu Gln Pro Leu Ile Phe Tyr Pro Gly		
450	455	460
Tyr Tyr Pro Asp Asp Asn Gly Ile Tyr Asn Gln Lys Phe Pro Phe Lys		
465	470	475
Thr Leu Ala Met Val Thr Ser Phe Leu Thr Asn Ile Cys Ile Ser Tyr		
485	490	495
Leu Ala Lys Tyr Leu Phe Glu Ser Gly Thr Leu Pro Pro Lys Leu Asp		
500	505	510
Val Phe Asp Ala Val Val Ala Arg His Ser Glu Glu Asn Met Asp Lys		
515	520	525
Thr Ile Leu Val Lys Asn Glu Asn Ile Lys Leu Asp Glu Leu Ala Leu		
530	535	540

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Val Lys Pro Arg Gln Ser Met Thr Leu Ser Ser Thr Phe Thr Asn Lys
545 550 555 560
Glu Ala Phe Leu Asp Val Asp Ser Ser Pro Glu Gly Ser Gly Thr Glu
565 570 575
Asp Asn Leu Gln
580

 $\langle 210 \rangle$ 7

<211> 1743

<212> DNA

<213> Mus musculus

 $\langle 220 \rangle$

<221> CDS

<222> (1)..(1743)

<400> 7

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ctt ata ttt ctg gtt gga ata tgg gct gca tgg aaa acc aaa aac agc 96
 Leu Ile Phe Leu Val Gly Ile Trp Ala Ala Trp Lys Thr Lys Asn Ser
 20 25 30

ggc aac cca gaa gag cac agt gaa gcc atc ata gtc ggg ggc cgt gac 144
Gly Asn Pro Glu Glu His Ser Glu Ala Ile Ile Val Gly Gly Arg Asp
35 40 45

att ggt ttg ttg gtt ggt ggt ttt acc atg aca gcc acc tgg gtt gga 192
Ile Gly Leu Leu Val Gly Gly Phe Thr Met Thr Ala Thr Trp Val Gly
50 55 60

gga ggc tac atc aat ggg aca gca gaa gca gtg tat ggg cca ggt tgt 240
 Gly Gly Tyr Ile Asn Gly Thr Ala Glu Ala Val Tyr Gly Pro Gly Cys
 65 70 75 80

ggt cta gct tgg gct cag gca ccc att gga tat tct ctg agt cta att 288
 Gly Leu Ala Trp Ala Gln Ala Pro Ile Gly Tyr Ser Leu Ser Leu Ile
 85 90 95

tta ggt ggt ctg ttt ttt gcg aaa cct atg cgt tcc aag gga tat gtg 336
 Leu Gly Gly Leu Phe Phe Ala Lys Pro Met Arg Ser Lys Gly Tyr Val
 100 105 110

act atg tta gac cca ttt caa cag atc tat gga aag cgc atg ggt ggg 384
 Thr Met Leu Asp Pro Phe Gln Gln Ile Tyr Gly Lys Arg Met Gly Gly
 115 120 125

ctg ctg ttc atc cct gca ctg atg gga gag atg ttc tgg gct gca gca 432
 Leu Leu Phe Ile Pro Ala Leu Met Gly Glu Met Phe Trp Ala Ala Ala
 130 135 140

att ttc tct gca tta ggg gcc acc atc agc gtg atc att gat gtg gat 480
 Ile Phe Ser Ala Leu Gly Ala Thr Ile Ser Val Ile Ile Asp Val Asp
 145 150 155 160

gtg aac ata tcg gtc att gtc tct gca ctg att gcc att ctt tat acc 528
 Val Asn Ile Ser Val Ile Val Ser Ala Leu Ile Ala Ile Leu Tyr Thr
 165 170 175

cta gtg ggt ggg ctg tac tct gtg gca tat act gat gtt gtc cag cta 576
 Leu Val Gly Gly Leu Tyr Ser Val Ala Tyr Thr Asp Val Val Gln Leu
 180 185 190

ttc tgc att ttt ata gga ctg tgg atc agt gtc cct ttt gcc ctg tca 624
 Phe Cys Ile Phe Ile Gly Leu Trp Ile Ser Val Pro Phe Ala Leu Ser
 195 200 205

cat cct gca gtc acc gac atc gga ttc aca gct gtg cat gct aaa tac 672
His Pro Ala Val Thr Asp Ile Gly Phe Thr Ala Val His Ala Lys Tyr

210

215

220

cag agt ccc tgg ctg gga acc att gaa tca gtt gaa gtc tac acc tgg 720
Gln Ser Pro Trp Leu Gly Thr Ile Glu Ser Val Glu Val Tyr Thr Trp

225

230

235

240

ctt gat aat ttt ctg tta ttg atg ctg ggt gga atc cca tgg caa gcc 768
Leu Asp Asn Phe Leu Leu Leu Met Leu Gly Gly Ile Pro Trp Gln Ala

245

250

255

tac ttc cag agg gtc ctc tct tca tcc tca gcc acc tat gct cag gta 816
Tyr Phe Gln Arg Val Leu Ser Ser Ser Ser Ala Thr Tyr Ala Gln Val

260

265

270

ctg tcc ttc ctg gca gct ttt ggg tgc ctg gtg atg gct cta ccc gcc 864
Leu Ser Phe Leu Ala Ala Phe Gly Cys Leu Val Met Ala Leu Pro Ala

275

280

285

ata tgc ata gga gct att gga gct tcc aca gac tgg aac cag act gcc 912
Ile Cys Ile Gly Ala Ile Gly Ala Ser Thr Asp Trp Asn Gln Thr Ala

290

295

300

tac ggg tat cca gat ccc aag act aag gag gaa gca gac atg att ctc 960
Tyr Gly Tyr Pro Asp Pro Lys Thr Lys Glu Glu Ala Asp Met Ile Leu

305

310

315

320

ccg atc gtt ctg cag tac ctc tgc cct gtg tac atc tcc ttc ttt ggg 1008
Pro Ile Val Leu Gln Tyr Leu Cys Pro Val Tyr Ile Ser Phe Phe Gly

325

330

335

ctt ggt gct gtt tca gct gct gtc atg tcc tca gct gac tgc tcc atc 1056
Leu Gly Ala Val Ser Ala Ala Val Met Ser Ser Ala Asp Ser Ser Ile

340	345	350	
ctg tcg gcg agt tct atg ttt gct cgg aat atc tac cag ctt tcc ttc			1104
Leu Ser Ala Ser Ser Met Phe Ala Arg Asn Ile Tyr Gln Leu Ser Phe			
355	360	365	
aga caa aat gca tca gac aag gaa att gtg tgg gtc atg agg atc act			1152
Arg Gln Asn Ala Ser Asp Lys Glu Ile Val Trp Val Met Arg Ile Thr			
370	375	380	
gtg ctt gtg ttc gga gca tct gca aca gcc atg gct ttg ctg acg aag			1200
Val Leu Val Phe Gly Ala Ser Ala Thr Ala Met Ala Leu Leu Thr Lys			
385	390	395	400
act gtg tat ggg ctc tgg tac ctg agc tct gac ctt gtc tac atc atc			1248
Thr Val Tyr Gly Leu Trp Tyr Leu Ser Ser Asp Leu Val Tyr Ile Ile			
405	410	415	
atc ttc cca cag ctg ctc tgt gta ctc ttc atc aaa gga acc aac act			1296
Ile Phe Pro Gln Leu Leu Cys Val Leu Phe Ile Lys Gly Thr Asn Thr			
420	425	430	
tat ggg gca gtt gct ggt tat att ttt gga cta ttc ctg aga att act			1344
Tyr Gly Ala Val Ala Gly Tyr Ile Phe Gly Leu Phe Leu Arg Ile Thr			
435	440	445	
gga gga gag cca tat cta tac ttg cag ccc tta atc ttc tac cct ggt			1392
Gly Gly Glu Pro Tyr Leu Tyr Leu Gln Pro Leu Ile Phe Tyr Pro Gly			
450	455	460	
tat tac tct gac aag aat ggt ata tac aat cag agg ttc cca ttt aaa			1440
Tyr Tyr Ser Asp Lys Asn Gly Ile Tyr Asn Gln Arg Phe Pro Phe Lys			
465	470	475	480
act ctc tcc atg gtt acc tca ttc ttt acc aac att tgt gtt tct tat			1488

Thr Leu Ser Met Val Thr Ser Phe Phe Thr Asn Ile Cys Val Ser Tyr
 485 490 495

cta gcc aag tat cta ttt gaa agt gga acc ttg cct cca aaa tta gat 1536
 Leu Ala Lys Tyr Leu Phe Glu Ser Gly Thr Leu Pro Pro Lys Leu Asp
 500 505 510

gta ttt gat gct gtt gtc gca agg cac agt gaa gag aac atg gac aag 1584
 Val Phe Asp Ala Val Val Ala Arg His Ser Glu Glu Asn Met Asp Lys
 515 520 525

acc att cta gtc aga aat gaa aat atc aaa tta aat gaa ctt gca cct 1632
 Thr Ile Leu Val Arg Asn Glu Asn Ile Lys Leu Asn Glu Leu Ala Pro
 530 535 540

gtg aaa cct cgg cag agc cta acc ctc agt tca act ttc acc aat aag 1680
 Val Lys Pro Arg Gln Ser Leu Thr Leu Ser Ser Thr Phe Thr Asn Lys
 545 550 555 560

gag gcc ctc ctt gat gtt gat tcc agt ccg gag ggg tct ggg act gaa 1728
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 565 570 575

gat aac tta caa tga 1743
 Asp Asn Leu Gln
 580

<210> 8

<211> 580

<212> PRT

<213> Mus musculus

<400> 8

Met Ser Phe His Val Glu Gly Leu Val Ala Ile Ile Leu Phe Tyr Leu

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 20 25 30
 Gly Asn Pro Glu Glu His Ser Glu Ala Ile Ile Val Gly Gly Arg Asp
 35 40 45
 Ile Gly Leu Leu Val Gly Gly Phe Thr Met Thr Ala Thr Trp Val Gly
 50 55 60
 Gly Gly Tyr Ile Asn Gly Thr Ala Glu Ala Val Tyr Gly Pro Gly Cys
 65 70 75 80
 Gly Leu Ala Trp Ala Gln Ala Pro Ile Gly Tyr Ser Leu Ser Leu Ile
 85 90 95
 Leu Gly Gly Leu Phe Phe Ala Lys Pro Met Arg Ser Lys Gly Tyr Val
 100 105 110
 Thr Met Leu Asp Pro Phe Gln Gln Ile Tyr Gly Lys Arg Met Gly Gly
 115 120 125
 Leu Leu Phe Ile Pro Ala Leu Met Gly Glu Met Phe Trp Ala Ala Ala
 130 135 140
 Ile Phe Ser Ala Leu Gly Ala Thr Ile Ser Val Ile Ile Asp Val Asp
 145 150 155 160
 Val Asn Ile Ser Val Ile Val Ser Ala Leu Ile Ala Ile Leu Tyr Thr
 165 170 175
 Leu Val Gly Gly Leu Tyr Ser Val Ala Tyr Thr Asp Val Val Gln Leu
 180 185 190
 Phe Cys Ile Phe Ile Gly Leu Trp Ile Ser Val Pro Phe Ala Leu Ser
 195 200 205
 His Pro Ala Val Thr Asp Ile Gly Phe Thr Ala Val His Ala Lys Tyr
 210 215 220
 Gln Ser Pro Trp Leu Gly Thr Ile Glu Ser Val Glu Val Tyr Thr Trp
 225 230 235 240
 Leu Asp Asn Phe Leu Leu Leu Met Leu Gly Gly Ile Pro Trp Gln Ala
 245 250 255
 Tyr Phe Gln Arg Val Leu Ser Ser Ser Ser Ala Thr Tyr Ala Gln Val
 260 265 270
 Leu Ser Phe Leu Ala Ala Phe Gly Cys Leu Val Met Ala Leu Pro Ala
 275 280 285

Ile Cys Ile Gly Ala Ile Gly Ala Ser Thr Asp Trp Asn Gln Thr Ala
 290 295 300
 Tyr Gly Tyr Pro Asp Pro Lys Thr Lys Glu Glu Ala Asp Met Ile Leu
 305 310 315 320
 Pro Ile Val Leu Gln Tyr Leu Cys Pro Val Tyr Ile Ser Phe Phe Gly
 325 330 335
 Leu Gly Ala Val Ser Ala Ala Val Met Ser Ser Ala Asp Ser Ser Ile
 340 345 350
 Leu Ser Ala Ser Ser Met Phe Ala Arg Asn Ile Tyr Gln Leu Ser Phe
 355 360 365
 Arg Gln Asn Ala Ser Asp Lys Glu Ile Val Trp Val Met Arg Ile Thr
 370 375 380
 Val Leu Val Phe Gly Ala Ser Ala Thr Ala Met Ala Leu Leu Thr Lys
 385 390 395 400
 Thr Val Tyr Gly Leu Trp Tyr Leu Ser Ser Asp Leu Val Tyr Ile Ile
 405 410 415
 Ile Phe Pro Gln Leu Leu Cys Val Leu Phe Ile Lys Gly Thr Asn Thr
 420 425 430
 Tyr Gly Ala Val Ala Gly Tyr Ile Phe Gly Leu Phe Leu Arg Ile Thr
 435 440 445
 Gly Gly Glu Pro Tyr Leu Tyr Leu Gln Pro Leu Ile Phe Tyr Pro Gly
 450 455 460
 Tyr Tyr Ser Asp Lys Asn Gly Ile Tyr Asn Gln Arg Phe Pro Phe Lys
 465 470 475 480
 Thr Leu Ser Met Val Thr Ser Phe Phe Thr Asn Ile Cys Val Ser Tyr
 485 490 495
 Leu Ala Lys Tyr Leu Phe Glu Ser Gly Thr Leu Pro Pro Lys Leu Asp
 500 505 510
 Val Phe Asp Ala Val Val Ala Arg His Ser Glu Glu Asn Met Asp Lys
 515 520 525
 Thr Ile Leu Val Arg Asn Glu Asn Ile Lys Leu Asn Glu Leu Ala Pro
 530 535 540
 Val Lys Pro Arg Gln Ser Leu Thr Leu Ser Ser Thr Phe Thr Asn Lys
 545 550 555 560
 Glu Ala Leu Leu Asp Val Asp Ser Ser Pro Glu Gly Ser Gly Thr Glu

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PCT/JP00/05545

565

570

575

Asp Asn Leu Gln

580